

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-1.n2p.raq.

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This page gives you Search Results detail for the Application 10618338 and Search Result us-10-618-338-1.n2p.raq.

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GenCore version 5.1.8
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OM nucleic - protein search, using frame plus n2p model

```
Run on:      May 25, 2006, 15:30:08 ; Search time 27 Seconds
              (without alignments)
              1630.739 Million cell updates/sec
```

```
Title:          US-10-618-338-1
Perfect score:  600
Sequence:       1 GACATTTCAGATGACCCAGTC.....GGACCAAGCTGGAGCTGAAA 321
```

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext 7.0
```

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 5179358

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10618338/runat_25052006_111814_26697/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10618338_@CGN_1_1_364_@runat_25052006_111814_26697 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

```
Database :      A_Geneseq_8:*
            1:  geneseqp1980s:*
```

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GenCore version 5.1.8
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 25, 2006, 15:41:33 ; Search time 7 Seconds
(without alignments)
1204.171 Million cell updates/sec

Title: US-10-618-338-1
Perfect score: 600
Sequence: 1 GACATTCAGATGACCCAGTC.....GGACCAAGCTGGAGCTGAAA 321

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 1301182

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10618338/runat_25052006_111822_26807/app_query.fasta_1
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10618338_@CGN_1_1_78_@runat_25052006_111822_26807
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 25, 2006, 15:42:33 ; Search time 24.2 Seconds
(without alignments)
1843.289 Million cell updates/sec

Title: US-10-618-338-1
Perfect score: 600
Sequence: 1 GACATTTCAGATGACCCAGTC.....GGACCAAGCTGGAGCTGAAA 321

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 4195594

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10618338/runat_25052006_111825_26857/app_query.fasta_1
-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10618338_@CGN_1_1_342_@runat_25052006_111825_26857 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 25, 2006, 15:43:53 ; Search time 1.7 Seconds
(without alignments)
630.897 Million cell updates/sec

Title: US-10-618-338-1
Perfect score: 600
Sequence: 1 GACATTCAGATGACCCAGTC.....GGACCAAGCTGGAGCTGAAA 321

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 112102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10618338/runat_25052006_111828_26908/app_query.fasta_1
-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10618338_@CGN_1_1_8_@runat_25052006_111828_26908 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA_New:*

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GenCore version 5.1.8
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 25, 2006, 15:35:08 ; Search time 5.6 Seconds
(without alignments)
1654.585 Million cell updates/sec

Title: US-10-618-338-1
Perfect score: 600
Sequence: 1 GACATTCAGATGACCCAGTC.....GGACCAAGCTGGAGCTGAAA 321

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10618338/runat_25052006_111819_26728/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10618338_CGN_1_1_63_runat_25052006_111819_26728 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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OM nucleic - protein search, using frame plus n2p model

```
Run on:      May 25, 2006, 15:30:23 ; Search time 38.4 Seconds
              (without alignments)
              2319.766 Million cell updates/sec
```

Title: US-10-618-338-1
Perfect score: 600
Sequence: 1 GACATTCAGATGACCCAGTC.....GGACCAAGCTGGAGCTGAAA 321

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext 7.0
```

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlpl
-Q=/abss/ABSSWEB_spool/US10618338/runat_25052006_111816_26708/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10618338_@CGN_1_1_612_@runat_25052006_111816_26708 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

```
Database :      UniProt_7.2:*
           1:  uniprot sprot:*
```

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OM protein - protein search, using sw model

Run on: May 25, 2006, 15:47:59 ; Search time 196 Seconds
(without alignments)
272.930 Million cell updates/sec

Title: US-10-618-338-4
Perfect score: 617
Sequence: 1 EIQLQQSGPELVKPGASVQV.....RDVTTALDFWGQGTTLTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GenCore version 5.1.8
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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 15:56:50 ; Search time 50 Seconds
              (without alignments)
              204.822 Million cell updates/sec
```

Title: US-10-618-338-4
Perfect score: 617
Sequence: 1 EIQLQQSGPELVKPGASVQV.....RDVTTALDFWCGQTTLTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Issued_Patents_AA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
--------	-------	-------	-------	--------	----	----	-------------

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 25, 2006, 15:57:29 ; Search time 181 Seconds
(without alignments)
299.426 Million cell updates/sec

Title: US-10-618-338-4
Perfect score: 617
Sequence: 1 EIQLQQSGPELVKPGASVQV.....RDVTTALDFWGQGTTLTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				Description
No.	Score	Match Length DB	ID			
<hr style="border-top: 1px dashed black;"/>						

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OM protein - protein search, using sw model

Run on: May 25, 2006, 15:58:24 ; Search time 15 Seconds
(without alignments)
86.871 Million cell updates/sec

Title: US-10-618-338-4
Perfect score: 617
Sequence: 1 EIQLQQSGPELVKPGASVQV.....RDVTTALDFWGQGTTTLTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	% Query
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 25, 2006, 15:51:49 ; Search time 38 Seconds
(without alignments)
296.246 Million cell updates/sec

Title: US-10-618-338-4
Perfect score: 617
Sequence: 1 EIQLQQSGPELVKPGASVQV.....RDVTTALDFWGQGTTLTVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	468.5	75.9	137	2 H32513	Ig heavy chain pre
2	465.5	75.4	139	2 A27609	Ig heavy chain pre
3	463	75.0	117	1 MHMS4E	Ig heavy chain V r
4	463	75.0	140	2 T01407	Ig heavy chain (my
5	461.5	74.8	128	2 I37267	Ig heavy chain V r
6	460	74.6	117	1 MHMSJ5	Ig heavy chain V r
7	452.5	73.3	119	2 F30502	Ig heavy chain V r
8	449	72.8	118	2 PL0200	anti-DNA autoantib

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-4.rup.

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 15:48:19 ; Search time 297 Seconds
              (without alignments)
              364.400 Million cell updates/sec
```

```
Title:          US-10-618-338-4
Perfect score:  617
Sequence:       1 EIQLQQSGPELVKPGASVQV.....RDVTTALDFWGQCTTLTVSS 117
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      UniProt_7.2:*
           1:  uniprot_sprot:*
           2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	476.5	77.2	481	2	Q8VCV5_MOUSE	Q8vcv5 mus musculu
2	475	77.0	117	2	Q9QXF0_MOUSE	Q9qxf0 mus musculu
3	474	76.8	117	2	Q9QXE9_MOUSE	Q9qxe9 mus musculu
4	470	76.2	134	2	Q65ZR6_MOUSE	Q65zr6 mus musculu

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-5.rag.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:01:34 ; Search time 76.8704 Seconds
(without alignments)
41.635 Million cell updates/sec

Title: US-10-618-338-5
Perfect score: 32
Sequence: 1 LASQTID 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:16 ; Search time 20.2222 Seconds
(without alignments)
30.299 Million cell updates/sec

Title: US-10-618-338-5
Perfect score: 32
Sequence: 1 LASQTID 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	32	100.0	7	1	US-08-814-806-5 Sequence 5, Appli
2	32	100.0	7	2	US-09-293-854-5 Sequence 5, Appli

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-5.ra

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:55 ; Search time 65.9815 Seconds
(without alignments)
49.143 Million cell updates/sec

Title: US-10-618-338-5
Perfect score: 32
Sequence: 1 LASQTID 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	32	100.0	7	3	US-09-293-854-5
2	32	100.0	7	3	US-09-990-586-5
3	32	100.0	7	4	US-10-293-417-5

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-5.rapbn.

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 16:31:10 ; Search time 3.37037 Seconds
              (without alignments)
              23.131 Million cell updates/sec
```

```
Title:      US-10-618-338-5
Perfect score: 32
Sequence:   1 LASQTID 7
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Published_Applications_AA_New:*
1:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

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A;Cross-references: UNIPROT:Q57532; UNIPARC:UPI000016FAEB; EMBL:Z70722; NID:e1059634; C;Accession: T08621 R;Mack, G.J.; Rees, J.; Sandblom, O.; Balczon, R.; Fritzler, M.J.; Rattner, J.B A;Experimental source: cell line HeLa Query Match 84.4%; Score 27; DB 2; Length 2442; Best Loc 2.5 through gene 9. A;Reference number: S07500; MUID:90133923; PMID:2614843 A;Accession: conserved hypothetical protein Atu2325 [imported] - Agrobacterium tumefaciens (strain C58, Dupc C.; Rouse, G.; Saenphimmachak, C.; Wu, Z.; Gordon, D.; Eisen, J.A.; Paulsen, I.; Karp, P.; Romer type: DNA A;Residues: 1-120 A;Cross-references: UNIPROT:Q8UD03; UNIPARC:UPI00000D1E6F; A84347 hypothetical protein Vng1962c [imported] - Halobacterium sp. NRC-1 C;Species: Halobact T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. S NID:g10581398; PIDN:AAG20141.1; GSPDB:GN00138 C;Genetics: A;Gene: VNG1962C Query Mat Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peter A82035; MUID:20406833; PMID:10952301 A;Accession: G82403 A;Status: preliminary A;Molecule Indels 0; Gaps 0; Qy 1 LASQTID 7 |||| || Db 206 LASQLID 212 RESULT 46 D49939 hypothetical pr A49939; MUID:94042918; PMID:8226689 A;Accession: D49939 A;Status: preliminary A;Molecule 1; Mismatches 0; Indels 0; Gaps 0; Qy 2 ASQTID 7 ||||| Db 36 ASQTLID 41 RESULT 47 I53142 ge RNAs. A;Reference number: I53142; MUID:94326666; PMID:8050375 A;Accession: I53142 A;Stat Db 80 LAGQTLID 86 RESULT 48 A47318 RNA-binding protein Raly - mouse C;Species: Mus musculu A;Molecule type: nucleic acid A;Residues: 1-296 A;Cross-references: UNIPARC:UPI0000022C47 A; horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004 C;Ac sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococc replaced by GenBank C;Genetics: A;Gene: PH1076 Query Match 81.2%; Score 26; DB 2; Length 3 L.; Wood, G.E.; Chen, Y.; Woo, L.; Kitajima, J.P.; Okura, V.K.; Almeida Jr., N.F.; Zhou, Y.; Bovee S.V.; Tomb, J.; Gordon, M.P.; Olson, M.V.; Nester, E.W. A;Title: The Genome of the Natural Genet 81.2%; Score 26; DB 2; Length 308; Best Local Similarity 85.7%; Pred. No. 1.9e+02; Matches 6;

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:14:40 ; Search time 11.6667 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-618-338-5
Perfect score: 32
Sequence: 1 LASQTID 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	283	2	S57134	hypothetical prote
2	30	93.8	401	2	E84757	hypothetical prote
3	29	90.6	387	1	S73618	MG372 homolog G12_
4	28	87.5	134	2	G69166	conserved hypothet
5	28	87.5	141	2	F64033	hypothetical prote
6	28	87.5	152	2	F82310	regulatory protein
7	28	87.5	179	2	T16996	ribonuclease (EC 3
8	28	87.5	264	2	H83859	dihydrodipicolinat
9	28	87.5	344	1	YFBSA	phenylalanine-tRNA
10	28	87.5	452	2	AI2966	hypothetical prote
11	28	87.5	452	2	B98316	thuE protein (AF17
12	28	87.5	704	2	S75260	hypothetical prote
13	28	87.5	817	2	T25758	hypothetical prote
14	28	87.5	819	2	B87580	conserved hypothet
15	28	87.5	831	2	H97801	translation initia
16	28	87.5	831	2	G71659	translation initia
17	28	87.5	1025	2	E86355	hypothetical prote
18	28	87.5	1751	2	T09394	gag-pro-pol polypr
19	27	84.4	75	2	T07511	photosystem II pho
20	27	84.4	76	2	F97241	glutaredoxin [impo
21	27	84.4	100	2	H38601	Ig kappa chain V r
22	27	84.4	198	2	B75149	thiamin biosynthes
23	27	84.4	201	2	B71189	hypothetical prote
24	27	84.4	293	2	E85363	hypothetical prote
25	27	84.4	341	2	B86633	tryptophan-tRNA li
26	27	84.4	357	2	H87378	phenylalanyl-tRNA
27	27	84.4	372	2	AD2111	twitching motility
28	27	84.4	374	1	G69359	conserved hypothet
29	27	84.4	381	2	B82840	conserved hypothet
30	27	84.4	425	2	AD2655	3-phosphoshikimate
31	27	84.4	425	2	H97436	3-phosphoshikimate
32	27	84.4	547	2	T40342	signal recognition
33	27	84.4	626	1	RGBY23	cell division cont
34	27	84.4	648	2	T34772	cell division prot
35	27	84.4	652	2	T19783	hypothetical prote
36	27	84.4	1000	2	T30280	hypothetical prote
37	27	84.4	1039	2	S76747	hypothetical prote
38	27	84.4	1070	2	H84369	isoleucyl-tRNA syn
39	27	84.4	1249	2	F86909	probable DNA gyras
40	27	84.4	1273	2	T10006	DNA topoisomerase
41	27	84.4	2442	2	T08621	centrosome associa
42	26	81.2	81	2	S07518	gene 6.5 protein -

43	26	81.2	120	2	AD2862	conserved hypothet
44	26	81.2	180	2	A84347	hypothetical prote
45	26	81.2	248	2	G82403	conserved hypothet
46	26	81.2	253	1	D49939	hypothetical prote
47	26	81.2	296	2	I53142	gene Merc protein
48	26	81.2	296	2	A47318	RNA-binding protei
49	26	81.2	303	2	A71102	hypothetical prote
50	26	81.2	308	2	AH2713	dehydrogenase Atul
51	26	81.2	322	2	AC1242	glucose kinase hom
52	26	81.2	322	2	AG1604	glucose kinase hom
53	26	81.2	327	1	SYECFA	phenylalanine-tRNA
54	26	81.2	327	2	AF0705	phenylalanyl-tRNA
55	26	81.2	327	2	E90931	phenylalanine tRNA
56	26	81.2	327	2	A85780	phenylalanine tRNA
57	26	81.2	327	2	C82225	phenylalanyl-tRNA
58	26	81.2	327	2	AE0296	phenylalanine-tRNA
59	26	81.2	334	2	E97495	D-galactose 1-dehy
60	26	81.2	339	2	A70677	probable fadE28 pr
61	26	81.2	365	2	T50566	probable ABC-type
62	26	81.2	414	2	B82408	hypothetical prote
63	26	81.2	417	2	E69804	multidrug resistan
64	26	81.2	425	2	T19415	hypothetical prote
65	26	81.2	444	2	T38760	hypothetical prote
66	26	81.2	460	2	C83468	conserved hypothet
67	26	81.2	483	2	I40031	uroporphyrin-III C
68	26	81.2	554	2	S46775	hypothetical prote
69	26	81.2	579	2	E90528	hypothetical prote
70	26	81.2	624	2	T26148	hypothetical prote
71	26	81.2	656	2	AE1479	probable cell surf
72	26	81.2	768	1	BVBY23	protein transport
73	26	81.2	827	2	A37849	S-layer protein -
74	26	81.2	881	1	A64040	hypothetical prote
75	26	81.2	891	2	S75940	methyl-accepting c
76	26	81.2	932	2	B70929	hypothetical prote
77	26	81.2	934	2	H88391	protein R06B10.2 [
78	26	81.2	949	2	T38543	hypothetical prote
79	26	81.2	960	2	S18240	phosphoenolpyruvat
80	26	81.2	967	2	JH0667	phosphoenolpyruvat
81	26	81.2	1081	2	T31094	surface antigen Bs
82	26	81.2	1093	2	A31758	phosphorylase kina
83	26	81.2	1093	2	B40793	phosphorylase kina
84	26	81.2	1181	2	T30578	myosin IC - slime
85	26	81.2	1242	2	D90186	reverse gyrase (to
86	26	81.2	1329	2	D87226	conserved hypothet
87	26	81.2	1330	2	B70836	hypothetical prote
88	26	81.2	1345	2	A87102	probable SpoIIIE-f
89	26	81.2	3429	2	T13853	hypothetical prote
90	25	78.1	105	2	S73207	ribosomal protein
91	25	78.1	107	2	F70537	hypothetical prote
92	25	78.1	111	2	C70024	nifU protein homol
93	25	78.1	120	2	S30770	ribosomal protein
94	25	78.1	145	2	AG2374	hypothetical prote
95	25	78.1	175	2	S37649	high-sulfur kerati
96	25	78.1	191	2	A43597	pilin type F9 prec
97	25	78.1	192	1	R5RT9	ribosomal protein
98	25	78.1	194	2	T06831	endopeptidase Clp
99	25	78.1	201	2	C95112	kinase, probable [
100	25	78.1	204	2	E83494	hypothetical prote
101	25	78.1	207	2	AE1925	cytochrome c oxida
102	25	78.1	210	2	A97981	conserved hypothet
103	25	78.1	241	2	JS0239	virG protein - Agr

104	25	78.1	243	2	T09769	uridylate kinase (
105	25	78.1	250	2	T31827	hypothetical prote
106	25	78.1	262	2	S62195	hypothetical prote
107	25	78.1	273	2	T06477	probable pyrroline
108	25	78.1	274	1	S10186	pyrroline-5-carbox
109	25	78.1	276	1	JQ2334	pyrroline-5-carbox
110	25	78.1	285	1	NDEC4	deoxyribonuclease
111	25	78.1	285	2	E85854	endonuclease IV [i
112	25	78.1	285	2	C91010	endonuclease IV [i
113	25	78.1	285	2	C84119	ATP synthase gamma
114	25	78.1	308	2	G98084	hypothetical prote
115	25	78.1	308	2	G95220	hypothetical prote
116	25	78.1	308	2	S11151	amiD protein - Str
117	25	78.1	324	2	AH1983	hypothetical prote
118	25	78.1	325	2	S32908	hypothetical prote
119	25	78.1	329	2	AG3055	succinoglycan bios
120	25	78.1	330	2	T14806	hypothetical prote
121	25	78.1	332	2	H90209	GTP-binding protei
122	25	78.1	337	2	F98230	succinoglycan bios
123	25	78.1	341	1	JS0340	anthranilate phosph
124	25	78.1	347	2	JC7178	chitinase (EC 3.2.
125	25	78.1	348	2	D95067	phenylalanyl-tRNA
126	25	78.1	352	2	F89884	Phe-tRNA synthetas
127	25	78.1	375	2	B81834	chorismate mutase
128	25	78.1	375	2	C97935	phenylalanine-tRNA
129	25	78.1	379	2	F90601	probable thiamin b
130	25	78.1	385	1	B64241	hypothetical prote
131	25	78.1	391	2	T20752	hypothetical prote
132	25	78.1	413	2	E96035	conserved hypothet
133	25	78.1	441	2	A40550	peroxisomal membra
134	25	78.1	461	2	A27672	hypothetical gag p
135	25	78.1	467	2	A57627	p55 erythrocyte me
136	25	78.1	482	2	T44628	probable transposa
137	25	78.1	503	2	S55589	D-nopaline dehydro
138	25	78.1	507	2	S64388	hypothetical prote
139	25	78.1	510	2	AB2782	long-chain fatty a
140	25	78.1	510	2	C97561	hypothetical prote
141	25	78.1	524	1	S76810	probable NADH2 deh
142	25	78.1	547	2	T23614	hypothetical prote
143	25	78.1	568	2	T17308	hypothetical prote
144	25	78.1	571	1	JN0858	chitinase (EC 3.2.
145	25	78.1	571	2	T42071	probable chitinase
146	25	78.1	581	2	E75383	conserved hypothet
147	25	78.1	694	2	D86615	polyribonucleotide
148	25	78.1	694	2	G72009	polyribonucleotide
149	25	78.1	708	2	T23616	hypothetical prote
150	25	78.1	733	2	S61984	probable membrane
151	25	78.1	739	2	T25030	hypothetical prote
152	25	78.1	827	2	S48465	6-phosphofructo-2-
153	25	78.1	833	2	S62136	CWH41 protein - ye
154	25	78.1	872	2	S51620	Ost oncogene - rat
155	25	78.1	888	2	H88085	protein T11F1.8 [i
156	25	78.1	901	1	WMNVTN	104K glycoprotein
157	25	78.1	903	2	T00358	hypothetical prote
158	25	78.1	961	2	AE2270	excinuclease ABC c
159	25	78.1	970	2	S77349	excinuclease ABC c
160	25	78.1	1044	2	H97186	glycosyltransferas
161	25	78.1	1177	2	I64233	hypothetical prote
162	25	78.1	1214	2	JC7259	Smad interacting p
163	25	78.1	1217	2	H82707	pilY1 protein homo
164	25	78.1	1230	2	F82857	PilY1 protein homo

165	25	78.1	1676	2	A56508	anucleate primary
166	25	78.1	1804	2	AI1850	serine/threonine k
167	25	78.1	2257	2	T09538	acetyl-CoA carboxy
168	25	78.1	2380	2	T29551	hypothetical prote
169	25	78.1	4385	2	T29042	hypothetical prote
170	24	75.0	42	2	H70246	hypothetical prote
171	24	75.0	42	2	F97915	choline binding pr
172	24	75.0	49	2	E85731	Rhs element associ
173	24	75.0	102	2	E97629	hypothetical prote
174	24	75.0	102	2	AG2852	hypothetical prote
175	24	75.0	104	2	H75402	conserved hypothet
176	24	75.0	107	2	H72764	hypothetical prote
177	24	75.0	110	2	S03174	pac protein - phag
178	24	75.0	111	2	PL0081	Ig kappa chain V r
179	24	75.0	124	2	A75374	hypothetical prote
180	24	75.0	131	2	JC5058	bitiscetin alpha c
181	24	75.0	146	2	T07125	plastid-lipid-asso
182	24	75.0	150	2	B83532	hypothetical prote
183	24	75.0	154	2	H86497	CT296 hypothetical
184	24	75.0	154	2	E72126	conserved hypothet
185	24	75.0	156	2	AB0561	probable membrane
186	24	75.0	157	1	G69782	conserved hypothet
187	24	75.0	160	2	AB1948	hypothetical prote
188	24	75.0	161	2	A69732	PBSX prophage ORF
189	24	75.0	168	2	T46100	hypothetical prote
190	24	75.0	179	2	AG3084	conserved hypothet
191	24	75.0	180	2	T16445	hypothetical prote
192	24	75.0	186	2	S76125	hypothetical prote
193	24	75.0	188	2	H82572	transposase XF2303
194	24	75.0	190	2	T39556	hypothetical prote
195	24	75.0	191	2	B98202	probable transcrip
196	24	75.0	194	1	YQEC7P	fimbrial protein 9
197	24	75.0	204	2	B75539	probable phosphogl
198	24	75.0	214	2	T18539	phosphoglycerate m
199	24	75.0	225	2	S76769	hypothetical prote
200	24	75.0	230	2	S76158	hypothetical prote
201	24	75.0	233	2	D69903	hypothetical prote
202	24	75.0	234	2	C89902	hypothetical prote
203	24	75.0	237	2	H86541	DNA polymerase III
204	24	75.0	237	2	A72083	DNA polymerase III
205	24	75.0	241	2	AF3327	transcription regu
206	24	75.0	242	2	A70710	hypothetical prote
207	24	75.0	243	2	T16605	hypothetical prote
208	24	75.0	249	2	C84270	30S ribosomal prot
209	24	75.0	249	2	S32609	phycoerythrin-asso
210	24	75.0	250	2	AB0421	PhnP protein [impo
211	24	75.0	253	2	AH3249	two component resp
212	24	75.0	253	2	S03760	virG protein - Agr
213	24	75.0	253	2	G90795	hypothetical prote
214	24	75.0	259	2	D97859	methionyl aminopep
215	24	75.0	259	2	A71644	methionine aminope
216	24	75.0	260	2	G84171	oxidoreductase [im
217	24	75.0	264	2	AH0574	ferric enterobacti
218	24	75.0	266	1	G41715	ribosomal protein
219	24	75.0	270	2	T03635	plastid-lipid-asso
220	24	75.0	275	2	D87459	conserved hypothet
221	24	75.0	276	2	G82436	probable thiosulfa
222	24	75.0	277	2	T38320	hypothetical prote
223	24	75.0	284	2	T15700	hypothetical prote
224	24	75.0	285	2	C95045	choline binding pr
225	24	75.0	291	2	AC2870	ABC transporter, m

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-5.rup.

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 16:01:54 ; Search time 93.8519 Seconds
              (without alignments)
              68.993 Million cell updates/sec
```

```
Title:      US-10-618-338-5
Perfect score: 32
Sequence:  1 LASQTID 7
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      UniProt_7.2:*
           1:  uniprot_sprot:*
           2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	32	100.0	283	1	YJ81_YEAST	P47148 saccharomyc
2	32	100.0	361	2	Q4Y5Y4_PLACH	Q4y5y4 plasmodium
3	32	100.0	403	2	Q48NE6_PSE14	Q48ne6 pseudomonas
4	32	100.0	611	2	Q94T96_9TELE	Q94t96 myctophum a

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:01:34 ; Search time 76.8704 Seconds
(without alignments)
41.635 Million cell updates/sec

Title: US-10-618-338-6
Perfect score: 33
Sequence: 1 AATNLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:16 ; Search time 20.2222 Seconds
(without alignments)
30.299 Million cell updates/sec

Title: US-10-618-338-6
Perfect score: 33
Sequence: 1 AATNLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	33	100.0	7	1	US-08-814-806-6
2	33	100.0	7	2	US-09-293-854-6

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-6.ra

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:55 ; Search time 65.9815 Seconds
(without alignments)
49.143 Million cell updates/sec

Title: US-10-618-338-6
Perfect score: 33
Sequence: 1 AATNLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	33	100.0	7	3	US-09-293-854-6
2	33	100.0	7	3	US-09-990-586-6
3	33	100.0	7	3	US-09-791-551-26

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:31:10 ; Search time 3.37037 Seconds
(without alignments)
23.131 Million cell updates/sec

Title: US-10-618-338-6
Perfect score: 33
Sequence: 1 AATNLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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A;Cross-references: UNIPARC:UPI00000D3B10; GB:Z95207; GB:AL123456; NID:g3261745; PIDN: (fragment) C;Species: Mus musculus (house mouse) C;Date: 29-Aug-1987 #sequence_revision 29 A;Residues: 1-71 A;Cross-references: UNIPARC:UPI0000115D36; GB:X03388; NID:g52171; PIDN: mouse) C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000 C;Acc UNIPARC:UPI000011517E; GB:M57988; NID:g196421; PIDN:AAA63368.1; PID:g196422 C;Superf. common tobacco (fragments) C;Species: Nicotiana tabacum (common tobacco) C;Date: 08-Dec-19 preliminary A;Molecule type: protein A;Residues: 1-109 A;Cross-references: UNIPROT:Q7M1Y2; UI influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;A Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995 A;Authors: Gneh GB:L42023; NID:g1574281; PIDN:AAC23101.1; PID:g1574291; TIGR:HI1453 C;Superfamily: Baci #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AC2648 R;Wood, D.W.; 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.; PIDN:AAL41601.1; PID:g17738938; GSPDB:GN00186 A;Experimental source: strain C58 (Dupont) #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: B97430 R;Goodner, B.; Biotechnology Agent Agrobacterium tumefaciens C58. A;Reference number: A97359; MUID:21608; Mismatches 0; Indels 0; Gaps 0; Qy 1 AATNLAD 7 |||:||| Db 37 AATSLAD 43 RESULT 20 A53191 h number: A53191; MUID:94170372; PMID:8124711 A;Accession: A53191 A;Status: preliminary A; protein - slime mold (Didymium iridis) C;Species: Didymium iridis C;Date: 06-Jan-1995 #sequence UNIPROT:Q07480; UNIPARC:UPI0000178A7F; EMBL:X71792 C;Superfamily: slime mold ribozyme Jul-2004 C;Accession: AI0199 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M. A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: / Length 371; Best Local Similarity 85.7%; Pred. No. 81; Matches 6; Conservative 1; Mismatches 0; M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Oku sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-416 A;Cross-refe Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 AATNLAD 7 || |||| Db 141 AAVNLAD 147 RE 1998 A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Ref C;Function: A;Description: may impart resistance to DNA alkylation C;Superfamily: DNA repair pro AATNLAD 7 |||| | Db 147 AATNLED 153 RESULT 25 T12203 transcription factor Vp1 - common ice A;Molecule type: mRNA A;Residues: 1-790 A;Cross-references: UNIPROT:O80394; UNIPARC:UPI0 C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_c Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. S iron receptor 1; tonB-dependent receptor amino-terminal homology; tonB-dependent receptor cart #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C;Accession: H70987 R;Cole, S.T.; Br S. Nature 393, 537-544, 1998 A;Authors: Sqaes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Bar A;Cross-references: UNIPROT:O06794; UNIPARC:UPI0000138EA7; GB:Z95890; GB:AL123456; NII (house shrew) C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 05-Oct-2004 protein A;Residues: 1-66 A;Cross-references: UNIPROT:P81497; UNIPARC:UPI00001315C1 C;Com 42 AATELAD 48 RESULT 29 AI0869 conserved hypothetical protein STY3178 [imported] - Salmonel Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dow MUID:21534947; PMID:11677608 A;Accession: AI0869 A;Status: preliminary A;Molecule type: DN B95116 hypothetical protein SP1007 [imported] - Streptococcus pneumoniae (strain TIGR4) C;Spe A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; I UNIPROT:Q97R32; UNIPARC:UPI000005169A; GB:AE005672; PIDN:AAK75123.1; PID:g14972480; C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C;Accession: H 5709-5717, 2001 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskuna Query Match 81.8%; Score 27; DB 2; Length 209; Best Local Similarity 85.7%; Pred. No. 76; Matc

Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welti, R.; Goo, Y.A.; Leithau
 Halobacterium species NRC-1. A;Reference number: A84160; MUID:20504483; PMID:11016950 A;
 Mismatches 1; Indels 0; Gaps 0; Qy 1 AATNLAD 7 ||| ||| Db 139 AATGLAD 145 RESULT 33 T35646
 GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-322 A;Cross-references: UNIPROT:Q9ZBR7; I
 H64143 hypothetical protein HI0146 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemo
 E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine,
 A;Residues: 1-329 A;Cross-references: UNIPROT:P44542; UNIPARC:UPI0000139362; GB:U32700;
 homolog, ubiquitin-like protein - fission yeast (*Schizosaccharomyces pombe*) C;Species: Schizosac
 UNIPARC:UPI000013A17B; EMBL:Z69240; PIDN:CAA93239.1; GSPDB:GN00066; SPDB:SPAC26A3
 names: protein D9954.7; protein YDR268w; tryptophanyl-tRNA synthetase C;Species: Saccharomy
 PIDN:AAB64452.1; PID:g1230641; GSPDB:GN00004; MIPS:YDR268w R;Entrup, R.; Langgut, W.; I
 15377, 1985 A;Title: MSW, a yeast gene coding for mitochondrial tryptophanyl-tRNA synthetase. A
 C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; mitochondrion; protein biosynthesis Query I
 A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; E
 Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.
 D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome
 homology Query Match 81.8%; Score 27; DB 2; Length 419; Best Local Similarity 85.7%; Pred. No
 M.; Tsagris, M. submitted to the EMBL Data Library, August 1993 A;Description: Structure and exp
 1118, 1995 A;Title: Structure and expression of LeMA-1, a tomato protein belonging to the SEC18-
 homology C;Keywords: ATP; nucleotide binding; P-loop F;184-394/Domain: FtsH/SEC18/CDC48-ty
 pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Dec-2002 (C
 Science 293, 498-506, 2001 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Doughert
 A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP2144 C;Superfamily: uncharacterized
 09-Dec-2002 C;Accession: E98115 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burge
 Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Rosteck Jr., P.R.; Skatrud, P.L.; Glass, J.I. A;Title: Genome
 Length 434; Best Local Similarity 85.7%; Pred. No. 1.7e+02; Matches 6; Conservative 0; Mismatch
 S.; Jagels, K.; Karlyshev, A.; Moule, S.; Pallen, M.J.; Penn, C.W.; Quail, M.; Rajandream, M.A.; Ru
 GB:AL111168; NID:g6967505; PIDN:CAB72573.1; PID:g6967583; GSPDB:GN00120; CJSP:Cj0089
 10-May-2001 #text_change 31-Dec-2004 C;Accession: H89251 R;anonymous, The C. elegans Seq
 1999 A;Accession: H89251 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-457 A;Cross
 43 A81722 glutamyl-tRNA(Gln) amidotransferase chain A TC0271 [imported] - Chlamydia muridar
 J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser, C.M. Nucleic Acids Res. 28, 1397-1406, 2000 A;
 source: strain Nigg (MoPn) C;Genetics: A;Gene: TC0271 C;Superfamily: indoleacetamide hydrolase
 C;Accession: F71568 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L
 GB:AE001273; NID:g3328388; PIDN:AAC67593.1; PID:g3328391 A;Experimental source: serotyp
 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_
 A;Residues: 1-492 A;Cross-references: UNIPROT:Q9Z9G7; UNIPARC:UPI000012B114; GB:AE0015
 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneu
 hydrolase Query Match 81.8%; Score 27; DB 2; Length 492; Best Local Similarity 100.0%; Pred. N
 Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishii, K.; Hattori, M.; Kuhara, S.; Nakazawa, T. Nucleic
 C;Genetics: A;Gene: gatA C;Superfamily: indoleacetamide hydrolase Query Match 81.8%; Score 2
 hydroxylase beta chain N;Contains: procollagen-proline dioxygenase (EC 1.14.11.2) beta chain; th
 A38362; MUID:90368750; PMID:1697592 A;Accession: A38362 A;Molecule type: mRNA A;Residue
 isomerase; thioredoxin homology C;Keywords: ascorbic acid; duplication; endoplasmic reticulum; I
 F;313-344/Disulfide bonds: #status predicted Query Match 81.8%; Score 27; DB 1; Length 509; B
 number: Z20390 A;Accession: T27588 A;Status: preliminary; translated from GB/EMBL/DDBJ A;M
 85.7%; Pred. No. 2.1e+02; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 AAT
 R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger
 A;Cross-references: UNIPROT:Q9I280; UNIPARC:UPI00000C5567; GB:AE004629; GB:AE004091; I
 AATNLAD 7 ||:|:| Db 57 AASNMAAD 63 RESULT 50 B41873 dnaK-type molecular chaperone dnaK -
 A;Reference number: A41873; MUID:92250425; PMID:1577695 A;Accession: B41873 A;Status: pr
 Similarity 71.4%; Pred. No. 2.4e+02; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:14:40 ; Search time 11.6667 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-618-338-6
Perfect score: 33
Sequence: 1 AATNLAD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			% Query		DB	ID	Description
	No.	Score	Match	Length			
1	33	100.0	77	2	G28840	Ig kappa chain V r	
2	33	100.0	81	2	S22024	Ig kappa chain - m	
3	33	100.0	84	2	E28840	Ig kappa chain V r	
4	33	100.0	843	2	S33442	EF protein - Strep	
5	33	100.0	1822	2	S33441	EF protein - Strep	
6	30	90.9	326	2	S36705	dUTP diphosphatase	
7	30	90.9	580	1	A34965	62K membrane antig	
8	30	90.9	580	1	S15577	62K membrane antig	
9	29	87.9	95	2	S26333	Ig kappa chain V r	
10	29	87.9	111	2	S24217	Ig kappa chain - m	
11	29	87.9	114	2	PT0358	Ig kappa chain V r	
12	29	87.9	383	2	T04427	hypothetical prote	
13	29	87.9	615	2	H70589	hypothetical glyci	
14	28	84.8	71	2	F28840	Ig kappa chain V r	
15	28	84.8	101	2	B37262	Ig kappa chain V r	
16	28	84.8	109	2	B32106	glucan endo-1,3-be	
17	28	84.8	156	2	D64124	regulatory protein	
18	28	84.8	175	2	AC2648	conserved hypothet	
19	28	84.8	185	2	B97430	hypothetical prote	
20	28	84.8	261	2	A53191	hypothetical prote	
21	28	84.8	261	2	S33356	hypothetical prote	

22	28	84.8	371	2	AI0199	tRNA (5-methylamin
23	28	84.8	416	2	S75793	poly(A) polymerase
24	28	84.8	448	1	A71659	DNA repair protein
25	28	84.8	790	2	T12203	transcription fact
26	28	84.8	851	2	D87252	TonB-dependent rec
27	28	84.8	914	2	H70987	hypothetical glyci
28	27	81.8	66	2	PC4360	pepsinogen A - hou
29	27	81.8	199	2	AI0869	conserved hypothet
30	27	81.8	209	2	B95116	hypothetical prote
31	27	81.8	209	2	H97985	hypothetical prote
32	27	81.8	232	2	A84276	hypothetical prote
33	27	81.8	322	2	T35646	probable thiamin m
34	27	81.8	329	2	H64143	hypothetical prote
35	27	81.8	354	2	T38404	yeast dsk2 homolog
36	27	81.8	379	1	YWBYM	tryptophan-tRNA li
37	27	81.8	419	2	C86223	hypothetical prote
38	27	81.8	423	2	S56672	probable 26S prote
39	27	81.8	426	2	H95250	conserved hypothet
40	27	81.8	434	2	E98115	conserved hypothet
41	27	81.8	453	2	A81425	probable lipoprote
42	27	81.8	457	2	H89251	protein ZC455.6 [i
43	27	81.8	491	2	A81722	glutamyl-tRNA(Gln)
44	27	81.8	491	2	F71568	probable glu-tRNA
45	27	81.8	492	2	H72130	glutamyl-tRNA(Gln)
46	27	81.8	492	2	C86491	Glu tRNA Gln amido
47	27	81.8	509	1	A38362	protein disulfide-
48	27	81.8	534	2	T27588	hypothetical prote
49	27	81.8	552	2	H83392	probable decarboxy
50	27	81.8	615	2	B41873	dnaK-type molecula
51	27	81.8	615	2	B97058	molecular chaperon
52	27	81.8	618	2	S22355	dnaK-type molecula
53	27	81.8	628	2	S73248	hypothetical prote
54	27	81.8	637	2	E69627	cell-division prot
55	27	81.8	648	2	T34772	cell division prot
56	27	81.8	657	2	E83660	cell-division prot
57	27	81.8	690	2	AE1464	cell division prot
58	27	81.8	691	2	AE1102	cell division prot
59	27	81.8	695	2	F84714	probable ftsH chlo
60	27	81.8	784	2	H75338	DNA helicase RecG
61	27	81.8	887	2	H96515	hypothetical prote
62	27	81.8	887	2	A96516	hypothetical prote
63	27	81.8	920	2	T41050	conserved hypothet
64	27	81.8	1453	2	G96613	hypothetical prote
65	27	81.8	1467	2	T48162	hypothetical prote
66	27	81.8	1560	2	T30282	calcium-binding pr
67	26	78.8	66	2	B39065	homeotic protein H
68	26	78.8	82	2	A56563	homeotic protein H
69	26	78.8	88	2	D37914	homeotic protein C
70	26	78.8	123	2	S57129	hypothetical prote
71	26	78.8	149	2	H75462	hypothetical prote
72	26	78.8	224	2	S28737	hypothetical prote
73	26	78.8	230	2	T31867	hypothetical prote
74	26	78.8	291	2	AC1302	hypothetical prote
75	26	78.8	291	2	AC1674	hypothetical prote
76	26	78.8	301	2	S35526	homeotic protein H
77	26	78.8	311	2	H83401	probable transcrip
78	26	78.8	321	1	E64026	probable S-adenosy
79	26	78.8	326	2	T42552	dUTP diphosphatase
80	26	78.8	331	2	F64047	D-2-hydroxy-acid d
81	26	78.8	333	2	A88504	protein B0361.5 [i
82	26	78.8	341	2	T51957	metalloproteinase

83	26	78.8	342	2	G84885	probable metallopr
84	26	78.8	344	2	A69507	conserved hypothet
85	26	78.8	345	2	E64115	thiamine-phosphate
86	26	78.8	367	2	A84998	hypothetical prote
87	26	78.8	376	2	A89957	hypothetical prote
88	26	78.8	418	2	G84164	hypothetical prote
89	26	78.8	418	2	C84360	potassium channel
90	26	78.8	430	2	C84190	tryptophan synthas
91	26	78.8	483	2	S45347	probable G protein
92	26	78.8	503	2	T39375	probable ATP-depen
93	26	78.8	515	2	S53525	G protein-coupled
94	26	78.8	551	2	F70684	hypothetical prote
95	26	78.8	561	2	T10046	hypothetical prote
96	26	78.8	571	1	S30253	GABA transport pro
97	26	78.8	571	2	F84956	acetolactate synth
98	26	78.8	573	2	E82072	acetolactate synth
99	26	78.8	574	2	G83059	acetolactate synth
100	26	78.8	575	2	C70781	probable fprB prot
101	26	78.8	675	2	AF0185	methionine-tRNA li
102	26	78.8	716	2	E82620	peptidyl-dipeptida
103	26	78.8	818	1	JC4397	peroxinectin precu
104	26	78.8	879	2	D96902	MDR-type permease
105	26	78.8	880	2	AF2128	hypothetical prote
106	26	78.8	913	2	T15278	hypothetical prote
107	26	78.8	1185	2	T36761	probable DNA polym
108	26	78.8	1201	2	A57369	anillin - fruit fl
109	26	78.8	1371	2	D82606	DNA primase XF2061
110	26	78.8	1558	2	B71603	RESA-H3 antigen PF
111	26	78.8	1795	2	D97312	hypothetical prote
112	26	78.8	2013	2	AD1129	probable peptidogl
113	26	78.8	2599	2	A96616	unknown protein F1
114	25	75.8	15	2	A56970	GLYMA1 - soybean (
115	25	75.8	79	2	A28840	Ig kappa chain V r
116	25	75.8	109	2	B70410	ybeB protein homol
117	25	75.8	113	2	AF1938	hypothetical prote
118	25	75.8	116	2	S20894	homeotic protein c
119	25	75.8	118	2	AE1753	Orf51 [bacteriopha
120	25	75.8	121	2	C36790	hypothetical prote
121	25	75.8	125	2	S05042	transcription fact
122	25	75.8	143	2	G71880	hypothetical prote
123	25	75.8	143	2	F64634	hypothetical prote
124	25	75.8	157	2	E97023	uncharacterized pr
125	25	75.8	166	2	H82263	phosphotyrosine pr
126	25	75.8	171	2	C97165	flagellar protein
127	25	75.8	179	2	A46447	hydrogenase-relate
128	25	75.8	182	2	AI0130	conserved hypothet
129	25	75.8	202	2	E95883	probable transcrip
130	25	75.8	220	2	AH2212	transport protein
131	25	75.8	221	2	C70704	probable rocD - My
132	25	75.8	223	2	T22911	hypothetical prote
133	25	75.8	233	2	JH0372	42K surface glycop
134	25	75.8	263	2	AD2821	tRNA/rRNA metyltra
135	25	75.8	268	2	B64318	hypothetical prote
136	25	75.8	273	2	H69206	dihydrodipicolinat
137	25	75.8	274	1	SUBSD	subtilisin (EC 3.4
138	25	75.8	276	2	T44319	hypothetical prote
139	25	75.8	279	2	G83837	pyrroline-5-carbox
140	25	75.8	281	2	AD2283	hypothetical prote
141	25	75.8	285	2	T27458	hypothetical prote
142	25	75.8	288	2	A89431	protein K02E2.5 [i
143	25	75.8	292	1	A40650	UTP-glucose-1-phos

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 16:01:54 ; Search time 93.8519 Seconds
              (without alignments)
              68.993 Million cell updates/sec
```

```
Title:      US-10-618-338-6
Perfect score: 33
Sequence:   1 AATNLAD 7
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      UniProt_7.2:*
           1:  uniprot_sprot:*
           2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	33	100.0	81	2	Q5R3T5_MOUSE	Q5r3t5 mus musculu
2	33	100.0	487	2	Q65ZL2_9MURI	Q65zl2 mus sp. fv/
3	33	100.0	514	2	Q64BG4_9ARCH	Q64bg4 uncultured
4	33	100.0	749	2	Q2WA97_MAGSA	Q2wa97 magnetospir

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:01:34 ; Search time 98.8333 Seconds
(without alignments)
41.635 Million cell updates/sec

Title: US-10-618-338-7
Perfect score: 47
Sequence: 1 QQVYSSPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:16 ; Search time 26 Seconds
(without alignments)
30.299 Million cell updates/sec

Title: US-10-618-338-7
Perfect score: 47
Sequence: 1 QQVYSSPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%
No.	Score Match Length DB ID	Description

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:55 ; Search time 84.8333 Seconds
(without alignments)
49.143 Million cell updates/sec

Title: US-10-618-338-7
Perfect score: 47
Sequence: 1 QQVYSSPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	100.0	9	3	US-09-293-854-7	Sequence 7, Appli
2	47	100.0	9	3	US-09-990-586-7	Sequence 7, Appli
3	47	100.0	9	4	US-10-293-417-7	Sequence 7, Appli

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:31:10 ; Search time 4.33333 Seconds
(without alignments)
23.131 Million cell updates/sec

Title: US-10-618-338-7
Perfect score: 47
Sequence: 1 QQVYSSPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:14:40 ; Search time 15 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-618-338-7
Perfect score: 47
Sequence: 1 QQVYSSPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	43	91.5	109	2 JN0296	Ig kappa chain V-J
2	38	80.9	109	2 S31981	Ig kappa chain - h
3	38	80.9	109	2 S32001	Ig kappa chain - h
4	38	80.9	109	2 S31983	Ig kappa chain - h
5	38	80.9	109	2 S31980	Ig kappa chain - h
6	38	80.9	109	2 S31979	Ig kappa chain - h
7	37	78.7	132	2 S46373	Ig kappa chain V-J
8	36	76.6	106	2 A49138	IgA kappa rheumato

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 16:01:54 ; Search time 120.667 Seconds
              (without alignments)
              68.993 Million cell updates/sec
```

```
Title:      US-10-618-338-7
Perfect score: 47
Sequence:   1 QQVYSSPFT 9
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      UniProt_7.2:*
           1:  uniprot_sprot:*
           2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	39	83.0	149	2	Q6D591_ERWCT	Q6d591 erwinia car
2	38	80.9	806	2	Q6AX43_XENLA	Q6ax43 xenopus lae
3	37	78.7	895	2	Q84UI6_ORYSA	Q84ui6 oryza sativ
4	37	78.7	895	2	Q8LLD6_ORYSA	Q8lld6 oryza sativ

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:01:34 ; Search time 65.8889 Seconds
(without alignments)
41.635 Million cell updates/sec

Title: US-10-618-338-8
Perfect score: 35
Sequence: 1 TDYNVY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 16:27:16 ; Search time 17.3333 Seconds
              (without alignments)
              30.299 Million cell updates/sec
```

```
Title:      US-10-618-338-8
Perfect score: 35
Sequence:   1 TDYNVY 6
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Issued_Patents_AA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:55 ; Search time 56.5556 Seconds
(without alignments)
49.143 Million cell updates/sec

Title: US-10-618-338-8
Perfect score: 35
Sequence: 1 TDYNVY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-8.rapbn.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:31:10 ; Search time 2.88889 Seconds
(without alignments)
23.131 Million cell updates/sec

Title: US-10-618-338-8
Perfect score: 35
Sequence: 1 TDYNVY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	% Query
--------	------------

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:14:40 ; Search time 10 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-618-338-8
Perfect score: 35
Sequence: 1 TDYNVY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	34	97.1	1225	1 S24284	E2 glycoprotein pr
2	34	97.1	1225	2 A36607	E2 glycoprotein -
3	34	97.1	1447	1 VGIHE3	E2 glycoprotein pr
4	34	97.1	1447	1 VGIHE2	E2 glycoprotein pr
5	34	97.1	1449	1 A43573	E2 glycoprotein pr
6	34	97.1	1449	1 VGIHFS	E2 glycoprotein pr
7	34	97.1	1449	2 S47423	E2 glycoprotein pr
8	34	97.1	1451	1 JQ1719	E2 glycoprotein pr

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 16:01:54 ; Search time 80.4444 Seconds
              (without alignments)
              68.993 Million cell updates/sec
```

Title: US-10-618-338-8
Perfect score: 35
Sequence: 1 TDYNVY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      UniProt_7.2:*
           1:  uniprot_sprot:*
           2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		Length	DB	ID	Description
		Query	Match				
1	35	100.0		240	2	Q4Y2U2_PLACH	Q4y2u2 plasmodium
2	35	100.0		333	2	Q9DGU2_YLDV	Q9dgu2 yaba-like d
3	35	100.0		724	2	Q61LQ7_CAEBR	Q61lq7 caenorhabdi
4	35	100.0		870	2	Q7R8W9_PLAYO	Q7r8w9 plasmodium

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:01:34 ; Search time 186.685 Seconds
(without alignments)
41.635 Million cell updates/sec

Title: US-10-618-338-9
Perfect score: 97
Sequence: 1 YIDPYNGITIYDQNFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:16 ; Search time 49.1111 Seconds
(without alignments)
30.299 Million cell updates/sec

Title: US-10-618-338-9
Perfect score: 97
Sequence: 1 YIDPYNGITIYDQNFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	97	100.0	17	1	US-08-814-806-9 Sequence 9, Appli

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:55 ; Search time 160.241 Seconds
(without alignments)
49.143 Million cell updates/sec

Title: US-10-618-338-9
Perfect score: 97
Sequence: 1 YIDPYNGITIYDQNFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:31:10 ; Search time 8.18519 Seconds
(without alignments)
23.131 Million cell updates/sec

Title: US-10-618-338-9
Perfect score: 97
Sequence: 1 YIDPYNGITIYDQNFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	% Query
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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:14:40 ; Search time 28.3333 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-618-338-9
Perfect score: 97
Sequence: 1 YIDPYNGITIYDQNFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	66	68.0	138	2	PH0105	anti-digoxin trans
2	65	67.0	120	2	A49982	Ig heavy chain V r
3	63	64.9	98	2	S17604	Ig heavy chain V r
4	63	64.9	107	2	S26320	Ig heavy chain V r
5	63	64.9	114	2	S26319	Ig heavy chain V r
6	63	64.9	135	2	PS0057	Ig heavy chain pre
7	63	64.9	139	2	A27609	Ig heavy chain pre
8	62	63.9	138	2	S45249	Ig heavy chain pre

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 16:01:54 ; Search time 227.926 Seconds
              (without alignments)
              68.993 Million cell updates/sec
```

Title: US-10-618-338-9
Perfect score: 97
Sequence: 1 YIDPYNGITIYDONFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      UniProt_7.2:*
           1:  uniprot_sprot:*
           2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	68	70.1	481	2	Q8VCV5_MOUSE	Q8vcv5 mus musculu
2	60	61.9	118	2	Q5R3X0_MOUSE	Q5r3x0 mus musculu
3	60	61.9	488	2	Q91WR1_MOUSE	Q91wrl1 mus musculu
4	57	58.8	120	2	Q920E8_MOUSE	Q920e8 mus musculu

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:01:34 ; Search time 87.8519 Seconds
(without alignments)
41.635 Million cell updates/sec

Title: US-10-618-338-10
Perfect score: 40
Sequence: 1 DVTTALDF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:16 ; Search time 23.1111 Seconds
(without alignments)
30.299 Million cell updates/sec

Title: US-10-618-338-10
Perfect score: 40
Sequence: 1 DVTTALDF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	40	100.0	8	1	US-08-814-806-10 Sequence 10, Appl
2	40	100.0	8	2	US-09-293-854-10 Sequence 10, Appl

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:27:55 ; Search time 75.4074 Seconds
(without alignments)
49.143 Million cell updates/sec

Title: US-10-618-338-10
Perfect score: 40
Sequence: 1 DVTTALDF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	100.0	8	3	US-09-293-854-10	Sequence 10, Appl
2	40	100.0	8	3	US-09-990-586-10	Sequence 10, Appl
3	40	100.0	8	4	US-10-293-417-10	Sequence 10, Appl
4	40	100.0	8	4	US-10-310-113-10	Sequence 10, Appl

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-10.rapbn.

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This page gives you Search Results detail for the Application 10618338 and Search Result us-10-618-338-10.rapbn.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:31:10 ; Search time 3.85185 Seconds
(without alignments)
23.131 Million cell updates/sec

Title: US-10-618-338-10
Perfect score: 40
Sequence: 1 DVTTALDF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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This page gives you Search Results detail for the Application 10618338 and Search Result us-10-6:
start

<http://es/ScoreAccessWeb/GetItem.action?AppId=10618338&seqId=523252&ItemName=...> 6/12/2006

15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T17947 R; 72.5%; Score 29; DB 2; Length 104; Best Local Similarity 62.5%; Pred. No. 38; Matches 5; Conse the T-DNA region from the Agrobacterium tumefaciens octopine Ti plasmid pTi15955. A;Reference No. 41; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Qy 1 DVTTALD 7 |:|||: Db 9 A;Cross-references: UNIPROT:Q20976; UNIPARC:UPI000007E14B; EMBL:Z74038; PIDN:CAA98498 Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sa Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VC1077 A;Map position: 1 Query F90532 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Dyl PIDN:CAC13339.1; GSPDB:GN00153 A;Experimental source: strain UAB CTIP C;Genetics: A;Gene: dioxygenase I C;Species: Rhodococcus globerulus C;Date: 25-May-1994 #sequence_revision 06-Ja references: UNIPROT:P47231; UNIPARC:UPI0000126926; GB:X75633; NID:g473115; PIDN:CAA53 one that exhibits homology with the corresponding proteins of analogous degradative pathways in Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 DVTTALDF 8 || |||| Db 153 DVD Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.A.; Theologis, A. submitt ATSP:T22J18.8 A;Map position: 1 A;Introns: 45/2; 62/3; 87/2; 121/2; 169/2; 186/3; 211/2; 235/ been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chang O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds A;Gene: STY2882 C;Superfamily: probable bacteriophage late gene regulator Query Match 72.5%; typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Dec-2002 C;Acces 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Steven C;Superfamily: probable bacteriophage late gene regulator Query Match 72.5%; Score 29; DB 2; L Consortium of the Organization for Nucleotide Sequencing and Analysis, Sao Paulo, Brazil. Nature 4 PIDN:AAF84267.1; GSPDB:GN00128; XFSC:XF1458 A;Experimental source: strain 9a5c R;Simpson Ferreira, A.J.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Monteiro Silva Jr., W.A.; da Silveira, J.F.; Silvestri, M.L.Z.; Siqueira, W.J.; de Souza, A.A.; de Souza, A.P.; T DVTASVDF 309 RESULT 48 D86177 protein F19P19.3 [imported] - Arabidopsis thaliana C;Species: Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hans Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P. references: UNIPROT:P93810; UNIPARC:UPI00000A4E0B; GB:AE005172; NID:g2341026; PIDN:AA #sequence_revision 14-May-1999 #text_change 09-Jul-2004 C;Accession: T07699 R;Bevan, M.; P ATSP:F17N18.80 A;Map position: 4 A;Introns: 32/1; 95/3; 159/1; 305/3 C;Superfamily: kinase-re #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 C;Accession: G86848 R;Bolotin, A.; V UNIPARC:UPI00000C6B0F; GB:AE005176; PID:g12724815; PIDN:AAK05889.1; GSPDB:GN00146 R

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OM protein - protein search, using sw model

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Run on:      May 25, 2006, 16:14:40 ; Search time 13.3333 Seconds
              (without alignments)
              57.730 Million cell updates/sec
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Title:          US-10-618-338-10
Perfect score:  40
Sequence:       1 DVTTALDF 8
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	34	85.0	366	2	AF1034
2	34	85.0	472	2	H81665
3	34	85.0	472	2	G71503
4	34	85.0	590	2	H84388
5	33	82.5	86	2	B87077
6	33	82.5	295	2	H91117
7	33	82.5	295	2	G85962
8	32	80.0	2710	2	A37052
9	31	77.5	108	2	F84357
10	31	77.5	146	2	AD2765
11	31	77.5	165	2	B97546
12	31	77.5	273	2	T49495
13	31	77.5	316	2	T46505
14	31	77.5	420	2	T02132
15	31	77.5	431	2	C89979
16	31	77.5	680	2	T08080
17	31	77.5	1518	2	T28880
18	31	77.5	2481	2	A43908
19	30	75.0	178	2	C72235
20	30	75.0	240	2	E70907
21	30	75.0	284	2	T35723
22	30	75.0	298	2	D95168
23	30	75.0	318	2	E98034
24	30	75.0	360	2	T03373
25	30	75.0	369	2	AG0224
26	30	75.0	397	2	F90449
27	30	75.0	397	2	B71242
28	30	75.0	529	2	F71547
29	30	75.0	601	2	JC5720
30	30	75.0	615	1	YUWTY
31	30	75.0	619	2	B97668
32	30	75.0	619	2	AG2892
33	30	75.0	690	2	E86442
34	30	75.0	1024	2	T05234
35	30	75.0	1168	2	H89816
36	30	75.0	1336	2	T02736
37	29	72.5	74	2	H70944
38	29	72.5	104	2	T17947
39	29	72.5	111	2	S28689
40	29	72.5	114	2	T22905

41	29	72.5	162	2	E82243	hypothetical prote
42	29	72.5	203	2	F90532	conserved hypothet
43	29	72.5	291	1	B53419	biphenyl-2,3-diol
44	29	72.5	316	2	T00769	hypothetical prote
45	29	72.5	366	2	AC0836	probable bacteriop
46	29	72.5	366	2	AE0930	probable regulator
47	29	72.5	398	2	G82677	conserved hypothet
48	29	72.5	399	2	D86177	protein F19P19.3 [
49	29	72.5	405	2	T07699	hypothetical prote
50	29	72.5	405	2	G86848	conserved hypothet
51	29	72.5	408	2	C95100	aminotransferase,
52	29	72.5	408	2	E97968	conserved hypothet
53	29	72.5	422	2	F90250	sugar phosphate nu
54	29	72.5	433	2	H84826	hypothetical prote
55	29	72.5	440	2	D84744	hypothetical prote
56	29	72.5	441	2	AG2237	hypothetical prote
57	29	72.5	476	2	AH2968	mannose-1-phosphat
58	29	72.5	476	2	C98314	mannose-1-phosphat
59	29	72.5	476	2	D71264	conserved hypothet
60	29	72.5	490	2	B71279	probable serine-ty
61	29	72.5	501	2	T35009	probable phospholi
62	29	72.5	523	1	S48997	IMP dehydrogenase
63	29	72.5	534	2	A98326	ketoglutarate semi
64	29	72.5	534	2	AE2957	dehydrogenase Atu3
65	29	72.5	541	2	H87696	DNA ligase, ATP-de
66	29	72.5	552	2	T30972	hypothetical prote
67	29	72.5	603	1	YUBHY	glycogen(starch) s
68	29	72.5	658	2	T33568	hypothetical prote
69	29	72.5	686	2	E87624	phospholipase C [i
70	29	72.5	705	2	B95843	probable catalase
71	29	72.5	707	2	H71375	probable 76K prote
72	29	72.5	776	2	T51911	related to protein
73	29	72.5	896	2	B81223	glutamate-ammonia-
74	29	72.5	896	2	E81994	probable [glutamat
75	29	72.5	1054	2	B75384	transcription-repa
76	29	72.5	1139	2	B70954	hypothetical prote
77	29	72.5	1152	2	D87046	conserved hypothet
78	29	72.5	1299	2	A86366	T26J12.6 protein -
79	29	72.5	1376	2	F83711	exopolygalacturona
80	29	72.5	1394	2	S66876	ATP-dependent tran
81	29	72.5	1430	2	T27924	hypothetical prote
82	29	72.5	1558	2	B71603	RESA-H3 antigen PF
83	28	70.0	65	2	B72172	H3R protein - vari
84	28	70.0	94	2	D70608	hypothetical prote
85	28	70.0	94	2	D70560	hypothetical prote
86	28	70.0	123	2	T03191	hypothetical prote
87	28	70.0	154	1	B64467	conserved hypothet
88	28	70.0	159	2	F87218	conserved hypothet
89	28	70.0	163	2	T24335	hypothetical prote
90	28	70.0	166	2	B70800	hypothetical prote
91	28	70.0	199	2	AI0869	conserved hypothet
92	28	70.0	253	2	S49183	hypothetical prote
93	28	70.0	292	2	H81417	hypothetical prote
94	28	70.0	294	2	G84940	dihydrodipicolinat
95	28	70.0	303	2	T35616	probable membrane
96	28	70.0	305	2	F69947	phage-related prot
97	28	70.0	307	2	AF3487	dienelactone hydro
98	28	70.0	310	2	G75615	hypothetical prote
99	28	70.0	316	2	S19389	hypothetical prote
100	28	70.0	323	2	AB3443	sua5 protein [impo
101	28	70.0	331	2	AC3141	conserved hypothet

102	28	70.0	337	2	D86463	hypothetical prote
103	28	70.0	341	2	F81276	probable sugar-pho
104	28	70.0	342	2	A97325	homolog of cell di
105	28	70.0	350	2	A42009	N-formyl peptide r
106	28	70.0	353	2	C70985	probable pks11 pro
107	28	70.0	353	2	H70694	probable histidino
108	28	70.0	357	2	A98147	hypothetical prote
109	28	70.0	358	1	S71887	serine/threonine-s
110	28	70.0	361	2	G75164	mannose-1-phosphat
111	28	70.0	365	2	T04319	polygalacturonase
112	28	70.0	380	2	G84373	tryptophanyl-tRNA
113	28	70.0	382	2	C85725	probable outer mem
114	28	70.0	382	2	F90892	probable outer mem
115	28	70.0	382	2	D64904	outer membrane ush
116	28	70.0	395	2	T23402	hypothetical prote
117	28	70.0	398	1	BWBY11	sporulation-specif
118	28	70.0	407	2	AC0971	conserved hypothet
119	28	70.0	412	2	T27202	hypothetical prote
120	28	70.0	414	2	T06367	gamma-glutamyl pho
121	28	70.0	429	2	H83191	enolase PA3635 [im
122	28	70.0	431	2	T45246	probable histidino
123	28	70.0	432	2	G64133	adenylosuccinate s
124	28	70.0	449	2	C87066	histidinol dehydro
125	28	70.0	450	2	T23528	hypothetical prote
126	28	70.0	450	2	T39088	probable vacuolar
127	28	70.0	461	2	T28006	hypothetical prote
128	28	70.0	470	2	T40020	probable protein t
129	28	70.0	474	2	AG3608	sensory transducti
130	28	70.0	478	2	T17225	hypothetical prote
131	28	70.0	482	2	C96962	penicillin-binding
132	28	70.0	530	2	B84130	two-component resp
133	28	70.0	541	2	T27107	hypothetical prote
134	28	70.0	568	2	T05060	hypothetical prote
135	28	70.0	572	2	T37128	hypothetical prote
136	28	70.0	575	2	D69512	acetolactate synth
137	28	70.0	580	1	EKECEX	gamma-glutamyltran
138	28	70.0	580	2	AB0994	gamma-glutamyltran
139	28	70.0	581	2	E91165	gamma-glutamyltran
140	28	70.0	581	2	E86011	gamma-glutamyltran
141	28	70.0	586	2	T19591	hypothetical prote
142	28	70.0	629	2	T05089	hypothetical prote
143	28	70.0	668	2	H71312	probable ATP-depen
144	28	70.0	683	2	I52996	transforming growt
145	28	70.0	702	2	A61619	arylphorin precurs
146	28	70.0	710	2	B71374	probable soluble l
147	28	70.0	734	2	AF3108	GGDEF family prote
148	28	70.0	747	2	F98178	nitrogen fixation
149	28	70.0	760	2	T41644	hypothetical trp-a
150	28	70.0	883	2	B85725	probable fimbrial
151	28	70.0	934	2	S75633	hypothetical prote
152	28	70.0	951	1	E64066	ribonuclease E (EC
153	28	70.0	1025	2	B86145	hypothetical prote
154	28	70.0	1226	2	I51617	kinesin-like prote
155	28	70.0	1261	2	G83162	respiratory nitrat
156	28	70.0	1264	2	A36858	G2R protein - vari
157	28	70.0	1282	2	T30804	P-glycoprotein 6 -
158	28	70.0	1423	2	A49206	exo-beta-D-fructos
159	28	70.0	1483	2	S30015	hypothetical prote
160	28	70.0	1511	2	S60932	probable membrane
161	28	70.0	1787	2	AC2009	serine/threonine k
162	28	70.0	1806	1	CGHU1E	collagen alpha 1(X

SCORE Search Results Details for Application 10618338 and Search Result us-10-618-338-10.rup.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 16:01:54 ; Search time 107.259 Seconds
(without alignments)
68.993 Million cell updates/sec

Title: US-10-618-338-10
Perfect score: 40
Sequence: 1 DVTTALDF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	92.5	408	2	Q37VU2_SPHAR	Q37vu2 novosphingo
2	35	87.5	208	2	Q3V457_MOUSE	Q3v457 mus musculu
3	35	87.5	413	1	MKNK1_RAT	Q4g050 rattus norv
4	35	87.5	415	2	Q3TDV2_MOUSE	Q3tdv2 mus musculu